

SEQUENCE LISTING

<110> Rosey, Everett L.
Strugnell, Richard A.
Good, Robert T,
King, Kendall W.

<120> NOVEL THERAPEUTIC COMPOSITIONS FOR
TREATING INFECTION BY LAWSONIA SPP.

<130> DAVI110.001AUS

<140> US 10/010,160

<141> 2001-11-09

<150> AU PR1381

<151> 2000-11-10

<150> US 60/249,596

<151> 2000-11-17

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<170> FastSEQ for Windows Version 4.0

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<212> DNA

<213> Lawsonia intracellularis

<220>

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cag gaa gct cgt tct gaa ggg agt gtc cct aaa tca gaa gag gtt act	96
Gln Glu Ala Arg Ser Glu Gly Ser Val Pro Lys Ser Glu Glu Val Thr	
20 25 30	
aaa gca ttg act act gca gca ggg atg ctg ggg ctt gct att tat tca	144
Lys Ala Leu Thr Thr Ala Ala Gly Met Leu Gly Leu Ala Ile Tyr Ser	
35 40 45	
ggc gta atg gga cgt cat ttt gaa aca att ttc tac tat att ttt aca	192
Gly Val Met Gly Arg His Phe Glu Thr Ile Phe Tyr Tyr Ile Phe Thr	
50 55 60	
gaa tca ttt cgg ttt gag gtt aca gca cag tca gta tat gct tta ttt	240
Glu Ser Phe Arg Phe Glu Val Thr Ala Gln Ser Val Tyr Ala Leu Phe	

65	70	75	80	
att tat gtt gct caa gag ata gct att tta ttg atg cca ata tta ctt				288
Ile Tyr Val Ala Gln Glu Ile Ala Ile Leu Leu Met Pro Ile Leu Leu	85	90	95	
ttt att gct gtt acg gca tgg att tca tta cgt gta caa gtt ggt gca				336
Phe Ile Ala Val Thr Ala Trp Ile Ser Leu Arg Val Gln Val Gly Ala	100	105	110	
tta tgg act aca aag gtt ttt aaa ttt aaa tgg agt aaa ttt aat ata				384
Leu Trp Thr Thr Lys Val Phe Lys Phe Lys Trp Ser Lys Phe Asn Ile	115	120	125	
ata aaa ggg ttg aaa gga atg ttt gct tct caa caa aca ctt gtt cga				432
Ile Lys Gly Leu Lys Gly Met Phe Ala Ser Gln Gln Thr Leu Val Arg	130	135	140	
ctt tta cgt agt tta gtt caa gta att gtt ata ggt att gtt cca tat				480
Leu Leu Arg Ser Leu Val Gln Val Ile Val Ile Gly Ile Val Pro Tyr	145	150	155	160
atg att ata aaa gga gag ttt tca aac ttt tta cca tta tat tat gca				528
Met Ile Ile Lys Gly Glu Phe Ser Asn Phe Leu Pro Leu Tyr Tyr Ala	165	170	175	
agt cct tca ggt gtg gca gat tat atg ctt aat aca gga ata gta ctt				576
Ser Pro Ser Gly Val Ala Asp Tyr Met Leu Asn Thr Gly Ile Val Leu	180	185	190	
gtt tta tat acg cta att cct atg aca att att gca gtc gca gat				621
Val Leu Tyr Thr Leu Ile Pro Met Thr Ile Ile Ala Val Ala Asp	195	200	205	
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Lys Ala Leu Thr Thr Ala Ala Gly Met Leu Gly Leu Ala Ile Tyr Ser				
35 40 45				
Gly Val Met Gly Arg His Phe Glu Thr Ile Phe Tyr Tyr Ile Phe Thr				
50 55 60				
Glu Ser Phe Arg Phe Glu Val Thr Ala Gln Ser Val Tyr Ala Leu Phe				
65 70 75 80				
Ile Tyr Val Ala Gln Glu Ile Ala Ile Leu Leu Met Pro Ile Leu Leu				
85 90 95				
Phe Ile Ala Val Thr Ala Trp Ile Ser Leu Arg Val Gln Val Gly Ala				

115	120	125	
ctt tat atg gtt gct aca tta gtt ttt ctt gct ctt aat ggc cat ttg			432
Leu Tyr Met Val Ala Thr Leu Val Phe Leu Ala Leu Asn Gly His Leu			
130	135	140	
ttt ctt ata aaa gct ttt aca tat act ttt aaa atg gtt cca gca gga			480
Phe Leu Ile Lys Ala Phe Thr Tyr Thr Phe Lys Met Val Pro Ala Gly			
145	150	155	160
gga ctt gtt gta aga gaa att tta ttg agt gaa ctt ctt aat atg gca			528
Gly Leu Val Val Arg Glu Ile Leu Leu Ser Glu Leu Leu Asn Met Ala			
	165	170	175
ggg atg att ttt gtt ttt gcc tta cat gtt gcg gca cca gtt atg tca			576
Gly Met Ile Phe Val Phe Ala Leu His Val Ala Ala Pro Val Met Ser			
	180	185	190
gct ctt ttt tta gta gag atc tct tta gga ctt atg gca aga gct gct			624
Ala Leu Phe Leu Val Glu Ile Ser Leu Gly Leu Met Ala Arg Ala Ala			
	195	200	205
cct cag att cat att atg gaa gtt gga ttt cct gta aaa att ggt gta			672
Pro Gln Ile His Ile Met Glu Val Gly Phe Pro Val Lys Ile Gly Val			
	210	215	220
gga ttt ttt ttc att gga cta tta ttt act atc tta tca aaa gaa acc			720
Gly Phe Phe Phe Ile Gly Leu Leu Phe Thr Ile Leu Ser Lys Glu Thr			
225	230	235	240
tat cga ttt att gca ggc cta gag gga cta ttt ttt aac tta ctt act			768
Tyr Arg Phe Ile Ala Gly Leu Glu Gly Leu Phe Phe Asn Leu Leu Thr			
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Val Met Gly Ser Gly Lys			
260			

<210> 4

<211> 262

<212> PRT

<213> Lawsonia intracellularis

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	20	25	30
Ile Asp Gly Phe Pro Asn Met Leu Lys Ala Ser Ile Ala Leu Ile Leu			
	35	40	45
Thr Ile Val Leu Trp Gly Arg Leu Ser Leu Ser Gly Thr Gln Met Pro			
	50	55	60
Ala His Pro Phe Asp Leu Val Leu Leu Ile Ile Ser Glu Val Phe Leu			
65	70	75	80

Gly	Ile	Val	Leu	Gly	Leu	Ala	Val	Asn	Phe	Phe	Phe	Ala	Gly	Ile	Gln
			85					90					95		
Ala	Gly	Gly	Glu	Ile	Leu	Ala	Thr	Gln	Met	Gly	Phe	Thr	Met	Ile	Thr
			100					105					110		
Leu	Ala	Asp	Pro	Leu	Thr	Gly	Asn	Thr	Thr	Gly	Phe	Ile	Ala	His	Phe
			115					120					125		
Leu	Tyr	Met	Val	Ala	Thr	Leu	Val	Phe	Leu	Ala	Leu	Asn	Gly	His	Leu
			130					135					140		
Phe	Leu	Ile	Lys	Ala	Phe	Thr	Tyr	Thr	Phe	Lys	Met	Val	Pro	Ala	Gly
															160
Gly	Leu	Val	Val	Arg	Glu	Ile	Leu	Leu	Ser	Glu	Leu	Leu	Asn	Met	Ala
															175
Gly	Met	Ile	Phe	Val	Phe	Ala	Leu	His	Val	Ala	Ala	Pro	Val	Met	Ser
															190
Ala	Leu	Phe	Leu	Val	Glu	Ile	Ser	Leu	Gly	Leu	Met	Ala	Arg	Ala	Ala
															205
Pro	Gln	Ile	His	Ile	Met	Glu	Val	Gly	Phe	Pro	Val	Lys	Ile	Gly	Val
															220
Gly	Phe	Phe	Phe	Ile	Gly	Leu	Leu	Phe	Thr	Ile	Leu	Ser	Lys	Glu	Thr
															240
Tyr	Arg	Phe	Ile	Ala	Gly	Leu	Glu	Gly	Leu	Phe	Phe	Asn	Leu	Leu	Thr
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Val	Met	Gly	Ser	Gly	Lys										
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1				5					10					15		
tca	ttg	aaa	gga	att	ttt	gaa	gat	gag	ggc	cat	gaa	gtt	tta	gaa	aga	96
Ser	Leu	Lys	Gly	Ile	Phe	Glu	Asp	Glu	Gly	His	Glu	Val	Leu	Glu	Arg	
			20						25				30			
gct	tca	gca	gaa	gaa	gga	ctt	aag	tgt	gtt	gat	gta	gag	tct	cca	gat	144
Ala	Ser	Ala	Glu	Glu	Gly	Leu	Lys	Cys	Val	Asp	Val	Glu	Ser	Pro	Asp	
			35					40				45				
ctt	gtt	ttt	ctt	gat	att	tgg	ctt	cct	ggg	atg	gat	ggt	ctt	atg	gct	192
Leu	Val	Phe	Leu	Asp	Ile	Trp	Leu	Pro	Gly	Met	Asp	Gly	Leu	Met	Ala	
			50				55				60					
tta	gac	cat	att	cag	gct	ctt	cat	cag	gaa	tta	cct	gtt	att	atg	att	240
Leu	Asp	His	Ile	Gln	Ala	Leu	His	Gln	Glu	Leu	Pro	Val	Ile	Met	Ile	
			65			70				75					80	

tca ggt cat gcc aca att gaa act gct gta aca gct atc cgt caa ggt	288
Ser Gly His Ala Thr Ile Glu Thr Ala Val Thr Ala Ile Arg Gln Gly	
85 90 95	
gct tat gat ttt att gaa aag cct ctt tct ttg gaa aaa gtc ctt att	336
Ala Tyr Asp Phe Ile Glu Lys Pro Leu Ser Leu Glu Lys Val Leu Ile	
100 105 110	
aca gct aat aga gct ata gaa aca gta aga tta aga agg gaa aac aaa	384
Thr Ala Asn Arg Ala Ile Glu Thr Val Arg Leu Arg Arg Glu Asn Lys	
115 120 125	
tta cta cgt act gta tta cct gag gag agt gag ttt ata gga cag tct	432
Leu Leu Arg Thr Val Leu Pro Glu Glu Ser Glu Phe Ile Gly Gln Ser	
130 135 140	
cct gtt atc tta aaa ttt aaa agt tta tta tca cag gtc gct cca aca	480
Pro Val Ile Leu Lys Phe Lys Ser Leu Leu Ser Gln Val Ala Pro Thr	
145 150 155 160	
gat gct tgg gta cta ctt aca gga gag aat ggt aca ggt aaa gag tta	528
Asp Ala Trp Val Leu Leu Thr Gly Glu Asn Gly Thr Gly Lys Glu Leu	
165 170 175	
gct gca caa gca ttg cac aaa gga agc tca cga tat caa aaa cca ttt	576
Ala Ala Gln Ala Leu His Lys Gly Ser Ser Arg Tyr Gln Lys Pro Phe	
180 185 190	
ata gct gtt aat tgt gct gct atc cct gaa gaa ttg att gaa agc gaa	624
Ile Ala Val Asn Cys Ala Ala Ile Pro Glu Glu Leu Ile Glu Ser Glu	
195 200 205	
cta ttt ggt cat gaa aaa ggg gcc ttt act ggt gcc gat gct tct cgt	672
Leu Phe Gly His Glu Lys Gly Ala Phe Thr Gly Ala Asp Ala Ser Arg	
210 215 220	
gca ggt cgt ttt gag ttg gca cat aaa gga aca tta ttt ctt gat gaa	720
Ala Gly Arg Phe Glu Leu Ala His Lys Gly Thr Leu Phe Leu Asp Glu	
225 230 235 240	
ata gga gat atg agt tta aaa aca caa gca aaa att ttg cgt att ttg	768
Ile Gly Asp Met Ser Leu Lys Thr Gln Ala Lys Ile Leu Arg Ile Leu	
245 250 255	
caa gaa caa tgt ttt gaa aaa att ggt agt gtt aga act att aaa gtt	816
Gln Glu Gln Cys Phe Glu Lys Ile Gly Ser Val Arg Thr Ile Lys Val	
260 265 270	
gat gta aga gtt att gca gca aca aat aag aat ctt gaa gac gct att	864
Asp Val Arg Val Ile Ala Ala Thr Asn Lys Asn Leu Glu Asp Ala Ile	
275 280 285	
agc gat gga aca ttt cgt caa gat ttg tat tat cgc tta cga gtt gtt	912
Ser Asp Gly Thr Phe Arg Gln Asp Leu Tyr Tyr Arg Leu Arg Val Val	

290	295	300	
cca ttg cat ctt ccc cct ctt cgt gaa cgt gat tct gat att gag cta			960
Pro Leu His Leu Pro Pro Leu Arg Glu Arg Asp Ser Asp Ile Glu Leu			
305	310	315	320
tta tta aat agg ttt gtg att cag ttg agt aaa cgt tat aga cgt gag			1008
Leu Leu Asn Arg Phe Val Ile Gln Leu Ser Lys Arg Tyr Arg Arg Glu			
	325	330	335
ccg cct att ttt tta gat gag gtc ttc cct gta ttg aaa caa tat tgt			1056
Pro Pro Ile Phe Leu Asp Glu Val Phe Pro Val Leu Lys Gln Tyr Cys			
	340	345	350
tgg cca ggg aat gta aga gaa tta ctt aat ttt gta gaa cga atg gtt			1104
Trp Pro Gly Asn Val Arg Glu Leu Leu Asn Phe Val Glu Arg Met Val			
	355	360	365
att ctt tat tca ggg aag aaa gta tgt ttg aca gat cct aag gta aaa			1152
Ile Leu Tyr Ser Gly Lys Lys Val Cys Leu Thr Asp Pro Lys Val Lys			
	370	375	380
agc aat tta aaa tat tta ccc aag aaa ttt tct tcc cat tat aac ttt			1200
Ser Asn Leu Lys Tyr Leu Pro Lys Lys Phe Ser Ser His Tyr Asn Phe			
	385	390	400
ctt ccc gat ata gat ttt aac cag gct aaa ata gct ttt gaa cca aaa			1248
Leu Pro Asp Ile Asp Phe Asn Gln Ala Lys Ile Ala Phe Glu Pro Lys			
	405	410	415
ttt tta act gaa aaa tta cat gct tat caa gga aat att acc cga tta			1296
Phe Leu Thr Glu Lys Leu His Ala Tyr Gln Gly Asn Ile Thr Arg Leu			
	420	425	430
gca gaa gct att gga ctt gaa aga agt tat tta tat aga aag cta aaa			1344
Ala Glu Ala Ile Gly Leu Glu Arg Ser Tyr Leu Tyr Arg Lys Leu Lys			
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agc tat ggt att tat ctg tct gag tga			1371
Ser Tyr Gly Ile Tyr Leu Ser Glu			
	450	455	

<210> 6

<211> 456

<212> PRT

<213> Lawsonia intracellularis

<400> 6

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			20				25					30			
Ala	Ser	Ala	Glu	Glu	Gly	Leu	Lys	Cys	Val	Asp	Val	Glu	Ser	Pro	Asp
		35					40					45			

Leu	Val	Phe	Leu	Asp	Ile	Trp	Leu	Pro	Gly	Met	Asp	Gly	Leu	Met	Ala	50	55	60
Leu	Asp	His	Ile	Gln	Ala	Leu	His	Gln	Glu	Leu	Pro	Val	Ile	Met	Ile	65	70	75
Ser	Gly	His	Ala	Thr	Ile	Glu	Thr	Ala	Val	Thr	Ala	Ile	Arg	Gln	Gly	85	90	95
Ala	Tyr	Asp	Phe	Ile	Glu	Lys	Pro	Leu	Ser	Leu	Glu	Lys	Val	Leu	Ile	100	105	110
Thr	Ala	Asn	Arg	Ala	Ile	Glu	Thr	Val	Arg	Leu	Arg	Arg	Glu	Asn	Lys	115	120	125
Leu	Leu	Arg	Thr	Val	Leu	Pro	Glu	Glu	Ser	Glu	Phe	Ile	Gly	Gln	Ser	130	135	140
Pro	Val	Ile	Leu	Lys	Phe	Lys	Ser	Leu	Leu	Ser	Gln	Val	Ala	Pro	Thr	145	150	155
Asp	Ala	Trp	Val	Leu	Leu	Thr	Gly	Glu	Asn	Gly	Thr	Gly	Lys	Glu	Leu	165	170	175
Ala	Ala	Gln	Ala	Leu	His	Lys	Gly	Ser	Ser	Arg	Tyr	Gln	Lys	Pro	Phe	180	185	190
Ile	Ala	Val	Asn	Cys	Ala	Ala	Ile	Pro	Glu	Glu	Leu	Ile	Glu	Ser	Glu	195	200	205
Leu	Phe	Gly	His	Glu	Lys	Gly	Ala	Phe	Thr	Gly	Ala	Asp	Ala	Ser	Arg	210	215	220
Ala	Gly	Arg	Phe	Glu	Leu	Ala	His	Lys	Gly	Thr	Leu	Phe	Leu	Asp	Glu	225	230	235
Ile	Gly	Asp	Met	Ser	Leu	Lys	Thr	Gln	Ala	Lys	Ile	Leu	Arg	Ile	Leu	245	250	255
Gln	Glu	Gln	Cys	Phe	Glu	Lys	Ile	Gly	Ser	Val	Arg	Thr	Ile	Lys	Val	260	265	270
Asp	Val	Arg	Val	Ile	Ala	Ala	Thr	Asn	Lys	Asn	Leu	Glu	Asp	Ala	Ile	275	280	285
Ser	Asp	Gly	Thr	Phe	Arg	Gln	Asp	Leu	Tyr	Tyr	Arg	Leu	Arg	Val	Val	290	295	300
Pro	Leu	His	Leu	Pro	Pro	Leu	Arg	Glu	Arg	Asp	Ser	Asp	Ile	Glu	Leu	305	310	315
Leu	Leu	Asn	Arg	Phe	Val	Ile	Gln	Leu	Ser	Lys	Arg	Tyr	Arg	Arg	Glu	325	330	335
Pro	Pro	Ile	Phe	Leu	Asp	Glu	Val	Phe	Pro	Val	Leu	Lys	Gln	Tyr	Cys	340	345	350
Trp	Pro	Gly	Asn	Val	Arg	Glu	Leu	Leu	Asn	Phe	Val	Glu	Arg	Met	Val	355	360	365
Ile	Leu	Tyr	Ser	Gly	Lys	Lys	Val	Cys	Leu	Thr	Asp	Pro	Lys	Val	Lys	370	375	380
Ser	Asn	Leu	Lys	Tyr	Leu	Pro	Lys	Lys	Phe	Ser	Ser	His	Tyr	Asn	Phe	385	390	395
Leu	Pro	Asp	Ile	Asp	Phe	Asn	Gln	Ala	Lys	Ile	Ala	Phe	Glu	Pro	Lys	405	410	415
Phe	Leu	Thr	Glu	Lys	Leu	His	Ala	Tyr	Gln	Gly	Asn	Ile	Thr	Arg	Leu	420	425	430
Ala	Glu	Ala	Ile	Gly	Leu	Glu	Arg	Ser	Tyr	Leu	Tyr	Arg	Lys	Leu	Lys	435	440	445
Ser	Tyr	Gly	Ile	Tyr	Leu	Ser	Glu									450	455	

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<211> 412
 <212> DNA
 <213> Lawsonia intracellularis

<220>
 <221> CDS
 <222> (1)...(411)

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 aat ctt caa gtc aat ttt tct aac cca tac cat caa aca gat att gaa 96
 Asn Leu Gln Val Asn Phe Ser Asn Pro Tyr His Gln Thr Asp Ile Glu
 20 25 30
 gtc ctg gct aat gca aaa aaa gtt aaa ggg atg aag ttt cca caa gac 144
 Val Leu Ala Asn Ala Lys Lys Val Lys Gly Met Lys Phe Pro Gln Asp
 35 40 45
 ttt aat aaa cct gaa gtt ata gtt gct ata cgt aat ggt agt aca gtt 192
 Phe Asn Lys Pro Glu Val Ile Val Ala Ile Arg Asn Gly Ser Thr Val
 50 55 60
 att act cct gca aag caa ctt ctt cct aaa gca tct ttt aga ctc ttt 240
 Ile Thr Pro Ala Lys Gln Leu Leu Pro Lys Ala Ser Phe Arg Leu Phe
 65 70 75 80
 gat gat gaa gtt gca tct ata aaa gat gta gaa tct gga caa tca cat 288
 Asp Asp Glu Val Ala Ser Ile Lys Asp Val Glu Ser Gly Gln Ser His
 85 90 95
 ata tta tta gct tca gca cca tta cca gcg att caa gct ata aac tca 336
 Ile Leu Leu Ala Ser Ala Pro Leu Pro Ala Ile Gln Ala Ile Asn Ser
 100 105 110
 aat ggc aac ctt att cgt tta gat aca ctc ccc att act cat caa tct 384
 Asn Gly Asn Leu Ile Arg Leu Asp Thr Leu Pro Ile Thr His Gln Ser
 115 120 125
 gta gga ttt gca ata aag aag gga gat c 412
 Val Gly Phe Ala Ile Lys Lys Gly Asp
 130 135

<210> 8
 <211> 137
 <212> PRT
 <213> Lawsonia intracellularis

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 Lys Gln Ile Asp Ile Ile Ile Ser Gly Ala Thr Ile Thr Leu Glu Arg
 1 5 10 15
 Asn Leu Gln Val Asn Phe Ser Asn Pro Tyr His Gln Thr Asp Ile Glu

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Val	Leu	Ala	Asn	Ala	Lys	Lys	Val	Lys	Gly	Met	Lys	Phe	Pro	Gln	Asp
	35		40		45										
Phe	Asn	Lys	Pro	Glu	Val	Ile	Val	Ala	Ile	Arg	Asn	Gly	Ser	Thr	Val
	50		55		60										
Ile	Thr	Pro	Ala	Lys	Gln	Leu	Leu	Pro	Lys	Ala	Ser	Phe	Arg	Leu	Phe
65			70		75									80	
Asp	Asp	Glu	Val	Ala	Ser	Ile	Lys	Asp	Val	Glu	Ser	Gly	Gln	Ser	His
			85		90									95	
Ile	Leu	Leu	Ala	Ser	Ala	Pro	Leu	Pro	Ala	Ile	Gln	Ala	Ile	Asn	Ser
			100		105									110	
Asn	Gly	Asn	Leu	Ile	Arg	Leu	Asp	Thr	Leu	Pro	Ile	Thr	His	Gln	Ser
			115		120									125	
Val	Gly	Phe	Ala	Ile	Lys	Lys	Gly	Asp							
	130						135								

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<211> 849

<212> DNA

<213> *Lawsonia intracellularis*

<220>

<221> CDS

<222> (1)...(846)

<400> 9

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1			5					10					15			
ggc	tac	ctt	atg	gct	aaa	ggg	aat	ctt	gct	tta	ctc	ttt	caa	cct	gca	96
Gly	Tyr	Leu	Met	Ala	Lys	Gly	Asn	Leu	Ala	Leu	Leu	Phe	Gln	Pro	Ala	
			20					25					30			
gaa	ctt	gtt	atc	att	att	ggg	gca	gca	tta	ggt	gct	ttt	ttt	gct	tca	144
Glu	Leu	Val	Ile	Ile	Ile	Gly	Ala	Ala	Leu	Gly	Ala	Phe	Phe	Ala	Ser	
			35					40					45			
cag	acg	aaa	tat	tca	ttt	act	ctg	gtc	att	aaa	aat	tta	tca	cac	att	192
Gln	Thr	Lys	Tyr	Ser	Phe	Thr	Leu	Val	Ile	Lys	Asn	Leu	Ser	His	Ile	
			50				55					60				
ttt	ggc	gat	cca	aac	agt	aca	aaa	ata	aaa	tac	ctt	gaa	aca	ctt	gcc	240
Phe	Gly	Asp	Pro	Asn	Ser	Thr	Lys	Ile	Lys	Tyr	Leu	Glu	Thr	Leu	Ala	
65					70					75				80		
ctt	ctc	tat	gga	ctt	ttc	tta	aaa	atg	aat	aga	gaa	ggt	gtc	att	agt	288
Leu	Leu	Tyr	Gly	Leu	Phe	Leu	Lys	Met	Asn	Arg	Glu	Gly	Val	Ile	Ser	
				85					90					95		
ata	gaa	agt	gat	ata	gaa	aaa	cct	gaa	tca	agt	cct	atc	ttt	agt	aaa	336
Ile	Glu	Ser	Asp	Ile	Glu	Lys	Pro	Glu	Ser	Ser	Pro	Ile	Phe	Ser	Lys	
				100				105					110			

tac cct aca att gta aaa gat act aaa gtt gtt gcc ttt att gca gat	384
Tyr Pro Thr Ile Val Lys Asp Thr Lys Val Val Ala Phe Ile Ala Asp	
115 120 125	
aca tta cga gtt tat ctg aca aca ggt gca cca gaa gat ata gat aac	432
Thr Leu Arg Val Tyr Leu Thr Thr Gly Ala Pro Glu Asp Ile Asp Asn	
130 135 140	
ctc atg gaa tct gac atg aaa att aca cac gaa gaa gaa tta tta cct	480
Leu Met Glu Ser Asp Met Lys Ile Thr His Glu Glu Glu Leu Leu Pro	
145 150 155 160	
gca cat tcc atc agc cat atg gca gag tcg cta cca gga atg ggt att	528
Ala His Ser Ile Ser His Met Ala Glu Ser Leu Pro Gly Met Gly Ile	
165 170 175	
gtt gct gca gta tta ggt gtt gtt att acc atg gga aaa att aat gag	576
Val Ala Ala Val Leu Gly Val Val Ile Thr Met Gly Lys Ile Asn Glu	
180 185 190	
cct cca gaa gtc ctt ggg cat tat att gga gca gct ttg gtt ggt aca	624
Pro Pro Glu Val Leu Gly His Tyr Ile Gly Ala Ala Leu Val Gly Thr	
195 200 205	
ttt ata ggt att ctt ttc tgt tat ggt ttt ttt gga cct atg ggt tca	672
Phe Ile Gly Ile Leu Phe Cys Tyr Gly Phe Phe Gly Pro Met Gly Ser	
210 215 220	
aag ctt gaa acc tct gca gaa gaa gca cat ttt tat tat aat tcc att	720
Lys Leu Glu Thr Ser Ala Glu Glu Ala His Phe Tyr Tyr Asn Ser Ile	
225 230 235 240	
aaa gaa gct gtt gca gct gct atc cga ggt tct aca cca atg ata gca	768
Lys Glu Ala Val Ala Ala Ala Ile Arg Gly Ser Thr Pro Met Ile Ala	
245 250 255	
gta gaa tat gga aga cgt gcc ata cct aat aca ttt cgt cca tca ttt	816
Val Glu Tyr Gly Arg Arg Ala Ile Pro Asn Thr Phe Arg Pro Ser Phe	
260 265 270	
tcg gaa atg gaa gaa cgt cta aaa aca gga taa	849
Ser Glu Met Glu Glu Arg Leu Lys Thr Gly	
275 280	

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<211> 282

<212> PRT

<213> Lawsonia intracellularis

<400> 10

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Gly Tyr Leu Met Ala Lys Gly Asn Leu Ala Leu Leu Phe Gln Pro Ala	
20 25 30	

aaa aca cct gat agt tcg cca atc tct aac aat cct ctt atc aac caa	192
Lys Thr Pro Asp Ser Ser Pro Ile Ser Asn Asn Pro Leu Ile Asn Gln	
50 55 60	
ata gat aaa ctt gat act cga caa tta aaa att aat gaa aca gaa caa	240
Ile Asp Lys Leu Asp Thr Arg Gln Leu Lys Ile Asn Glu Thr Glu Gln	
65 70 75 80	
tct cat tat gct ctt gct aat aaa tta aaa aaa atg tta atg gct gat	288
Ser His Tyr Ala Leu Ala Asn Lys Leu Lys Lys Met Leu Met Ala Asp	
85 90 95	
gct atc cca cag tca gca aca gga ata agt gct gac gat gtt ggt gta	336
Ala Ile Pro Gln Ser Ala Thr Gly Ile Ser Ala Asp Asp Val Gly Val	
100 105 110	
tta tta cgt gta aat tct aat tcc acg ttt ttt cct ggt aca gca act	384
Leu Leu Arg Val Asn Ser Asn Ser Thr Phe Phe Pro Gly Thr Ala Thr	
115 120 125	
ctt aca ccc gaa ggg aaa aaa gtt atg gga act gtt tta gcc gtt ctc	432
Leu Thr Pro Glu Gly Lys Lys Val Met Gly Thr Val Leu Ala Val Leu	
130 135 140	
cgt gaa tat aat ctt tac ctt gtg ata cgt ggc cat gct gat att ggt	480
Arg Glu Tyr Asn Leu Tyr Leu Val Ile Arg Gly His Ala Asp Ile Gly	
145 150 155 160	
gaa ata aca aaa ggc agc cct ttt gct tct aac tgg gaa ctt tca gga	528
Glu Ile Thr Lys Gly Ser Pro Phe Ala Ser Asn Trp Glu Leu Ser Gly	
165 170 175	
gct cgt gca gct gca gct gca cag tat ctt gta gag cac ggg ata aag	576
Ala Arg Ala Ala Ala Ala Ala Gln Tyr Leu Val Glu His Gly Ile Lys	
180 185 190	
gct tca cga att cgc tct gta gga tat gca gat aca aga cct cta gaa	624
Ala Ser Arg Ile Arg Ser Val Gly Tyr Ala Asp Thr Arg Pro Leu Glu	
195 200 205	
cct agt tct cct gaa gga agt aca aaa aat cgt cgt ata gaa ttc tat	672
Pro Ser Ser Pro Glu Gly Ser Thr Lys Asn Arg Arg Ile Glu Phe Tyr	
210 215 220	
ttt cat cgg cca gaa gtt atg tct tat ggc gtt gta tat taa	714
Phe His Arg Pro Glu Val Met Ser Tyr Gly Val Val Tyr *	
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<400> 12

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			20					25					30		
Val	Lys	Glu	Gly	Leu	Ala	Ala	Tyr	Phe	Ser	Ser	Ser	Asp	Ala	Thr	Phe
		35					40					45			
Lys	Thr	Pro	Asp	Ser	Ser	Pro	Ile	Ser	Asn	Asn	Pro	Leu	Ile	Asn	Gln
	50					55					60				
Ile	Asp	Lys	Leu	Asp	Thr	Arg	Gln	Leu	Lys	Ile	Asn	Glu	Thr	Glu	Gln
65					70					75					80
Ser	His	Tyr	Ala	Leu	Ala	Asn	Lys	Leu	Lys	Lys	Met	Leu	Met	Ala	Asp
				85					90					95	
Ala	Ile	Pro	Gln	Ser	Ala	Thr	Gly	Ile	Ser	Ala	Asp	Asp	Val	Gly	Val
			100					105					110		
Leu	Leu	Arg	Val	Asn	Ser	Asn	Ser	Thr	Phe	Phe	Pro	Gly	Thr	Ala	Thr
		115					120					125			
Leu	Thr	Pro	Glu	Gly	Lys	Lys	Val	Met	Gly	Thr	Val	Leu	Ala	Val	Leu
	130					135					140				
Arg	Glu	Tyr	Asn	Leu	Tyr	Leu	Val	Ile	Arg	Gly	His	Ala	Asp	Ile	Gly
145					150					155					160
Glu	Ile	Thr	Lys	Gly	Ser	Pro	Phe	Ala	Ser	Asn	Trp	Glu	Leu	Ser	Gly
				165					170					175	
Ala	Arg	Ala	Ala	Ala	Ala	Ala	Gln	Tyr	Leu	Val	Glu	His	Gly	Ile	Lys
			180					185					190		
Ala	Ser	Arg	Ile	Arg	Ser	Val	Gly	Tyr	Ala	Asp	Thr	Arg	Pro	Leu	Glu
		195					200					205			
Pro	Ser	Ser	Pro	Glu	Gly	Ser	Thr	Lys	Asn	Arg	Arg	Ile	Glu	Phe	Tyr
	210					215					220				
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Met	Ile	Ile	Leu	Leu	Gly	Thr	Val	Phe	Leu	Ile	Val	Leu	Ile	Ser	Ala	
1				5					10					15		
tta	tgc	tca	atg	atg	gaa	gct	gct	ata	tac	tct	atc	cct	att	act	tat	96
Leu	Cys	Ser	Met	Met	Glu	Ala	Ala	Ile	Tyr	Ser	Ile	Pro	Ile	Thr	Tyr	
			20					25				30				
att	gaa	cac	ctt	cgt	gaa	cag	gga	agc	aaa	aaa	gga	gaa	aaa	ctt	tat	144
Ile	Glu	His	Leu	Arg	Glu	Gln	Gly	Ser	Lys	Lys	Gly	Glu	Lys	Leu	Tyr	
		35					40					45				

tat tta cat agt aat att gat cag cct att aca gcc gta tta ata ttg	192
Tyr Leu His Ser Asn Ile Asp Gln Pro Ile Thr Ala Val Leu Ile Leu	
50 55 60	
aat act ata gca aat act gct gga gct gcc ctt gct gga gca att gct	240
Asn Thr Ile Ala Asn Thr Ala Gly Ala Ala Leu Ala Gly Ala Ile Ala	
65 70 75 80	
aca aca aca ctt cat gaa tct act aag cct ttc ttt gca gca atc ctc	288
Thr Thr Thr Leu His Glu Ser Thr Lys Pro Phe Phe Ala Ala Ile Leu	
85 90 95	
acc ttg ctt att tta gct ttt ggg gaa att ata cct aaa aca cta ggt	336
Thr Leu Leu Ile Leu Ala Phe Gly Glu Ile Ile Pro Lys Thr Leu Gly	
100 105 110	
gtt gct tac tct aaa cgt att gct ata att ctc ctt aat cct ctc tct	384
Val Ala Tyr Ser Lys Arg Ile Ala Ile Ile Leu Leu Asn Pro Leu Ser	
115 120 125	
att ctt ata gtt act tta aaa ccc ctt att atg ctt tca agc tac tta	432
Ile Leu Ile Val Thr Leu Lys Pro Leu Ile Met Leu Ser Ser Tyr Leu	
130 135 140	
aca cga ctt gtt tca cct cga aaa cgt cct aca gtt aca gaa gat gac	480
Thr Arg Leu Val Ser Pro Arg Lys Arg Pro Thr Val Thr Glu Asp Asp	
145 150 155 160	
atc cgt gca ctt aca agt ctt tcc aga gag tct ggt cgt att aag cca	528
Ile Arg Ala Leu Thr Ser Leu Ser Arg Glu Ser Gly Arg Ile Lys Pro	
165 170 175	
tat gaa gaa cat gtc ata aaa aat atc ctt agt ctt gat tta aaa tat	576
Tyr Glu Glu His Val Ile Lys Asn Ile Leu Ser Leu Asp Leu Lys Tyr	
180 185 190	
gct cat gaa att atg act ccc aga act atg gtc ttt tca ctt cat gaa	624
Ala His Glu Ile Met Thr Pro Arg Thr Met Val Phe Ser Leu His Glu	
195 200 205	
aac ctt act gtc tct gaa gct tat agc aac ccc aaa ata tgg aac tat	672
Asn Leu Thr Val Ser Glu Ala Tyr Ser Asn Pro Lys Ile Trp Asn Tyr	
210 215 220	
agt cgc atc cct act tat gga gaa aat aac gaa gac att act ggc att	720
Ser Arg Ile Pro Thr Tyr Gly Glu Asn Asn Glu Asp Ile Thr Gly Ile	
225 230 235 240	
atc caa cga tat gaa att gga cga tat atg acc aat gga gaa aca gaa	768
Ile Gln Arg Tyr Glu Ile Gly Arg Tyr Met Thr Asn Gly Glu Thr Glu	
245 250 255	
aaa aaa ctt tta gaa att atg caa cca gca aaa ttt gtc ctt gaa agt	816
Lys Lys Leu Leu Glu Ile Met Gln Pro Ala Lys Phe Val Leu Glu Ser	

260	265	270	
caa act gta gat cat tta ctt ctt gca ttt tta gaa gaa aga caa cat			864
Gln Thr Val Asp His Leu Leu Leu Ala Phe Leu Glu Glu Arg Gln His			
275	280	285	
ctt ttt att gta ctt gat gag tat ggg gga tta tct ggt gtt gtt tcc			912
Leu Phe Ile Val Leu Asp Glu Tyr Gly Gly Leu Ser Gly Val Val Ser			
290	295	300	
tta gaa gat gta tta gaa act atg ctt gga aga gaa att gtt gat gaa			960
Leu Glu Asp Val Leu Glu Thr Met Leu Gly Arg Glu Ile Val Asp Glu			
305	310	315	320
agt gat aca aca cct gat ctt aga gca ctt gca aaa aaa aga cat agt			1008
Ser Asp Thr Thr Pro Asp Leu Arg Ala Leu Ala Lys Lys Arg His Ser			
325	330	335	
gca tta atc caa aat aat aaa aat act ctt tta aaa taa			1047
Ala Leu Ile Gln Asn Asn Lys Asn Thr Leu Leu Lys			
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<211> 348

<212> PRT

<213> Lawsonia intracellularis

<400> 14

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			20					25					30		
Ile	Glu	His	Leu	Arg	Glu	Gln	Gly	Ser	Lys	Lys	Gly	Glu	Lys	Leu	Tyr
		35				40						45			
Tyr	Leu	His	Ser	Asn	Ile	Asp	Gln	Pro	Ile	Thr	Ala	Val	Leu	Ile	Leu
		50				55					60				
Asn	Thr	Ile	Ala	Asn	Thr	Ala	Gly	Ala	Ala	Leu	Ala	Gly	Ala	Ile	Ala
65					70					75				80	
Thr	Thr	Thr	Leu	His	Glu	Ser	Thr	Lys	Pro	Phe	Phe	Ala	Ala	Ile	Leu
				85				90						95	
Thr	Leu	Leu	Ile	Leu	Ala	Phe	Gly	Glu	Ile	Ile	Pro	Lys	Thr	Leu	Gly
			100				105						110		
Val	Ala	Tyr	Ser	Lys	Arg	Ile	Ala	Ile	Ile	Leu	Leu	Asn	Pro	Leu	Ser
		115					120					125			
Ile	Leu	Ile	Val	Thr	Leu	Lys	Pro	Leu	Ile	Met	Leu	Ser	Ser	Tyr	Leu
		130				135				140					
Thr	Arg	Leu	Val	Ser	Pro	Arg	Lys	Arg	Pro	Thr	Val	Thr	Glu	Asp	Asp
145					150					155				160	
Ile	Arg	Ala	Leu	Thr	Ser	Leu	Ser	Arg	Glu	Ser	Gly	Arg	Ile	Lys	Pro
				165					170					175	
Tyr	Glu	Glu	His	Val	Ile	Lys	Asn	Ile	Leu	Ser	Leu	Asp	Leu	Lys	Tyr
			180					185					190		
Ala	His	Glu	Ile	Met	Thr	Pro	Arg	Thr	Met	Val	Phe	Ser	Leu	His	Glu
		195					200					205			

Asn	Leu	Thr	Val	Ser	Glu	Ala	Tyr	Ser	Asn	Pro	Lys	Ile	Trp	Asn	Tyr
210						215					220				
Ser	Arg	Ile	Pro	Thr	Tyr	Gly	Glu	Asn	Asn	Glu	Asp	Ile	Thr	Gly	Ile
225						230					235				240
Ile	Gln	Arg	Tyr	Glu	Ile	Gly	Arg	Tyr	Met	Thr	Asn	Gly	Glu	Thr	Glu
				245						250					255
Lys	Lys	Leu	Leu	Glu	Ile	Met	Gln	Pro	Ala	Lys	Phe	Val	Leu	Glu	Ser
			260						265						270
Gln	Thr	Val	Asp	His	Leu	Leu	Leu	Ala	Phe	Leu	Glu	Glu	Arg	Gln	His
		275						280							285
Leu	Phe	Ile	Val	Leu	Asp	Glu	Tyr	Gly	Gly	Leu	Ser	Gly	Val	Val	Ser
	290					295					300				
Leu	Glu	Asp	Val	Leu	Glu	Thr	Met	Leu	Gly	Arg	Glu	Ile	Val	Asp	Glu
305						310				315					320
Ser	Asp	Thr	Thr	Pro	Asp	Leu	Arg	Ala	Leu	Ala	Lys	Lys	Arg	His	Ser
				325					330						335
Ala	Leu	Ile	Gln	Asn	Asn	Lys	Asn	Thr	Leu	Leu	Lys				
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Met	Gln	Lys	Val	Cys	Tyr	Phe	Phe	Leu	Ile	Thr	Phe	Phe	Tyr	Phe	Phe	
1				5					10					15		
ata aca gaa aat tat ctc ttt gct aca tca att acc act tcc aca att															96	
Ile	Thr	Glu	Asn	Tyr	Leu	Phe	Ala	Thr	Ser	Ile	Thr	Thr	Ser	Thr	Ile	
			20					25					30			
aac caa caa cat ata gca tat aca gtt act ttt acc tct cca gaa aat															144	
Asn	Gln	Gln	His	Ile	Ala	Tyr	Thr	Val	Thr	Phe	Thr	Ser	Pro	Glu	Asn	
			35				40					45				
cct aat ctt gca aca gag atg gaa aca cat agt gaa tta gta aag ctt															192	
Pro	Asn	Leu	Ala	Thr	Glu	Met	Glu	Thr	His	Ser	Glu	Leu	Val	Lys	Leu	
		50				55					60					
gca aat caa tct tta gat agt aaa ata ggt tta aat tta cgt gtt aaa															240	
Ala	Asn	Gln	Ser	Leu	Asp	Ser	Lys	Ile	Gly	Leu	Asn	Leu	Arg	Val	Lys	
		65			70				75					80		
gaa gat ata agt aca gca caa aaa att ctt gac tcg aat ggt tat tat															288	
Glu	Asp	Ile	Ser	Thr	Ala	Gln	Lys	Ile	Leu	Asp	Ser	Asn	Gly	Tyr	Tyr	
				85				90						95		
agt gga agt gtc gag gga aag att gac tgg cag acg aac cct att agt															336	

Ser	Gly	Ser	Val	Glu	Gly	Lys	Ile	Asp	Trp	Gln	Thr	Asn	Pro	Ile	Ser	
			100					105					110			
atc	caa	atc	caa	ttt	aaa	cca	aat	gta	caa	tat	aaa	ata	aat	aca	ata	384
Ile	Gln	Ile	Gln	Phe	Lys	Pro	Asn	Val	Gln	Tyr	Lys	Ile	Asn	Thr	Ile	
			115					120					125			
cat	atc	caa	tac	ctt	gat	agt	gaa	ctt	gca	tat	ctc	cct	ctt	tcc	tta	432
His	Ile	Gln	Tyr	Leu	Asp	Ser	Glu	Leu	Ala	Tyr	Leu	Pro	Leu	Ser	Leu	
			130					135					140			
gaa	gaa	ttc	aat	ctc	tct	aaa	ggc	aat	cct	gct	ctt	gct	gtt	aat	atc	480
Glu	Glu	Phe	Asn	Leu	Ser	Lys	Gly	Asn	Pro	Ala	Leu	Ala	Val	Asn	Ile	
						150				155					160	
cta	tcc	tct	gta	agt	agc	ctc	atg	caa	tat	ata	cat	aat	aat	gga	tat	528
Leu	Ser	Ser	Val	Ser	Ser	Leu	Met	Gln	Tyr	Ile	His	Asn	Asn	Gly	Tyr	
						165				170					175	
cca	tta	gcc	aaa	ata	aaa	aaa	act	caa	tac	ata	att	aat	cgg	atg	gat	576
Pro	Leu	Ala	Lys	Ile	Lys	Lys	Thr	Gln	Tyr	Ile	Ile	Asn	Arg	Met	Asp	
			180							185				190		
tat	aca	ttt	gat	att	gat	tta	gta	ata	aga	caa	gga	ccg	tta	ctc	cat	624
Tyr	Thr	Phe	Asp	Ile	Asp	Leu	Val	Ile	Arg	Gln	Gly	Pro	Leu	Leu	His	
			195					200					205			
atg	ggc	aaa	gta	caa	cct	caa	cat	aat	ctc	aat	att	tca	aca	ata	ttc	672
Met	Gly	Lys	Val	Gln	Pro	Gln	His	Asn	Leu	Asn	Ile	Ser	Thr	Ile	Phe	
			210					215				220				
cta	aat	aaa	att	gct	aca	tgg	aag	gaa	gga	agg	gta	tgg	aac	aat	gca	720
Leu	Asn	Lys	Ile	Ala	Thr	Trp	Lys	Glu	Gly	Arg	Val	Trp	Asn	Asn	Ala	
						230				235					240	
ctc	ctt	gat	tct	tat	cga	aca	cgg	ctt	caa	caa	aca	ggc	ctt	ttc	agt	768
Leu	Leu	Asp	Ser	Tyr	Arg	Thr	Arg	Leu	Gln	Gln	Thr	Gly	Leu	Phe	Ser	
						245				250				255		
tct	ata	act	ctc	aat	cca	agg	aat	caa	aaa	gaa	caa	aat	ggc	aac	acc	816
Ser	Ile	Thr	Leu	Asn	Pro	Arg	Asn	Gln	Lys	Glu	Gln	Asn	Gly	Asn	Thr	
						260				265				270		
tct	ata	gaa	ctt	gtt	gca	aca	gaa	gcc	cct	cca	agg	act	att	agt	ggc	864
Ser	Ile	Glu	Leu	Val	Ala	Thr	Glu	Ala	Pro	Pro	Arg	Thr	Ile	Ser	Gly	
						275				280				285		
ggc	tta	caa	tac	tct	tct	gat	caa	ggc	att	ggc	gca	cgt	ggg	act	tgg	912
Gly	Leu	Gln	Tyr	Ser	Ser	Asp	Gln	Gly	Ile	Gly	Ala	Arg	Gly	Thr	Trp	
						290					300					
gaa	cat	cga	aat	gtt	ttt	ggc	aat	gga	gaa	ctt	ttt	cgt	ata	aca	gca	960
Glu	His	Arg	Asn	Val	Phe	Gly	Asn	Gly	Glu	Leu	Phe	Arg	Ile	Thr	Ala	
						310				315					320	

cca ata agt cga gat gat caa aaa att atg gca aac ttc caa aaa cca	1008
Pro Ile Ser Arg Asp Asp Gln Lys Ile Met Ala Asn Phe Gln Lys Pro	
325 330 335	
gcc ttt ggc cgt cca aat caa tca tta att agt gaa gca caa ctt aaa	1056
Ala Phe Gly Arg Pro Asn Gln Ser Leu Ile Ser Glu Ala Gln Leu Lys	
340 345 350	
aaa gaa aat aca aaa agt tac aaa caa caa ctt gca tct att gct tta	1104
Lys Glu Asn Thr Lys Ser Tyr Lys Gln Gln Leu Ala Ser Ile Ala Leu	
355 360 365	
gga att gaa cga caa ttt aat aga cgt tgg ttt ggt agt agc agt ctt	1152
Gly Ile Glu Arg Gln Phe Asn Arg Arg Trp Phe Gly Ser Ser Ser Leu	
370 375 380	
tca gtt gat aca gga ttt atg gat gat cga gat tct ata aaa aaa ata	1200
Ser Val Asp Thr Gly Phe Met Asp Asp Arg Asp Ser Ile Lys Lys Ile	
385 390 395 400	
ttt act ctt ttt ggc atc ccc tta tca ata aca agg gat agt tct aaa	1248
Phe Thr Leu Phe Gly Ile Pro Leu Ser Ile Thr Arg Asp Ser Ser Lys	
405 410 415	
gat cct ctt aat cct atc caa gga aca aaa gct acc tta aat gtt act	1296
Asp Pro Leu Asn Pro Ile Gln Gly Thr Lys Ala Thr Leu Asn Val Thr	
420 425 430	
cct tat att ggt aaa tat aaa aaa aag att ttg act tta cgt agt cgg	1344
Pro Tyr Ile Gly Lys Tyr Lys Lys Lys Ile Leu Thr Leu Arg Ser Arg	
435 440 445	
ttt gat ttt agc ttt tac ata gac gtt ctt aaa aca ggg aaa ctt atc	1392
Phe Asp Phe Ser Phe Tyr Ile Asp Val Leu Lys Thr Gly Lys Leu Ile	
450 455 460	
ttg gct aac aaa ata gca ata ggt tcc ctc cta ggg aaa gat ata gaa	1440
Leu Ala Asn Lys Ile Ala Ile Gly Ser Leu Leu Gly Lys Asp Ile Glu	
465 470 475 480	
aac tat cct gca ata cta agg ttt tat gct ggg ggt ggt ggt agt gta	1488
Asn Tyr Pro Ala Ile Leu Arg Phe Tyr Ala Gly Gly Gly Gly Ser Val	
485 490 495	
aga ggg tat gac tat caa tca ttg gga cca aaa aat aaa tat ggg gat	1536
Arg Gly Tyr Asp Tyr Gln Ser Leu Gly Pro Lys Asn Lys Tyr Gly Asp	
500 505 510	
gct att gga gga ctt tct ttt tca act att agt ttt gaa tta cga tta	1584
Ala Ile Gly Gly Leu Ser Phe Ser Thr Ile Ser Phe Glu Leu Arg Leu	
515 520 525	
aaa ata aca gaa tcc att ggc att gtg cca att tat tgg atg ggg gaa	1632
Lys Ile Thr Glu Ser Ile Gly Ile Val Pro Ile Tyr Trp Met Gly Glu	
530 535 540	

tat tta cga aaa aaa aat ttc ctg act tta aaa aaa tca ata tat tgg 1680
Tyr Leu Arg Lys Lys Asn Phe Leu Thr Leu Lys Lys Ser Ile Tyr Trp
545 550 555 560

tta gat ata gca act cca ctt caa gat aga agc cat aat aaa cac ttt 1776
Leu Asp Ile Ala Thr Pro Leu Gln Asp Arg Ser His Asn Lys His Phe
580 585 590

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1 5 10 15	
 gca ttt acg tta ttt tta gga ctt att att aca ggc att ctt ttt ata	96
Ala Phe Thr Leu Phe Leu Gly Leu Ile Ile Thr Gly Ile Leu Phe Ile	
20 25 30	
 cgg acc tct aca ggc att gct tgg att aaa aat aca gtt tct tct tta	144
Arg Thr Ser Thr Gly Ile Ala Trp Ile Lys Asn Thr Val Ser Ser Leu	
35 40 45	
 ctt caa caa caa gga att ata cta caa gta tct tca att att gga cca	192
Leu Gln Gln Gln Gly Ile Ile Leu Gln Val Ser Ser Ile Ile Gly Pro	
50 55 60	
 ttc cca gaa caa att act att aat gaa ctt agc ctt agt gat gtg aat	240
Phe Pro Glu Gln Ile Thr Ile Asn Glu Leu Ser Leu Ser Asp Val Asn	
65 70 75 80	
 gga act tac ctt aca ata tct aac tta gaa atc caa tca aac tta tgg	288
Gly Thr Tyr Leu Thr Ile Ser Asn Leu Glu Ile Gln Ser Asn Leu Trp	
85 90 95	
 gct tta ttc aaa ggt caa ctt gaa att ctg tct ttt gaa ctt aat gat	336
Ala Leu Phe Lys Gly Gln Leu Glu Ile Leu Ser Phe Glu Leu Asn Asp	
100 105 110	
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Leu Val Leu Tyr Arg Leu Pro Ser Asn Asn Asn Leu Lys Lys Ser Ser	
115 120 125	
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Thr Ser Phe Val Leu Pro His Ile Ser Phe Asp Leu Thr Pro Trp Trp	
130 135 140	
 act gaa cat att cgt att caa aac atc cat att aac aat aca caa ctt	480
Thr Glu His Ile Arg Ile Gln Asn Ile His Ile Asn Asn Thr Gln Leu	
145 150 155 160	
 tcc tct gat att ata ggt att cca ttg gta tta tcc ctt gag ggt gat	528
Ser Ser Asp Ile Ile Gly Ile Pro Leu Val Leu Ser Leu Glu Gly Asp	
165 170 175	
 ggt aca tta aca aat tgg aat gga aca ttt caa cta tcc tct tct aac	576
Gly Thr Leu Thr Asn Trp Asn Gly Thr Phe Gln Leu Ser Ser Ser Asn	
180 185 190	
 aaa aca aaa att ata gga acg ctt cgt tac caa ggg aat aag aca caa	624
Lys Thr Lys Ile Ile Gly Thr Leu Arg Tyr Gln Gly Asn Lys Thr Gln	
195 200 205	
 ttt ttt gaa tat gtt cat cct aca cgg ata gta aca cta gag ata gac	672

Phe	Phe	Glu	Tyr	Val	His	Pro	Thr	Arg	Ile	Val	Thr	Leu	Glu	Ile	Asp	
210						215					220					
agc	gta	gct	gat	aaa	aag	tca	tat	aat	aat	agt	atc	ctt	gaa	caa	cct	720
Ser	Val	Ala	Asp	Lys	Lys	Ser	Tyr	Asn	Asn	Ser	Ile	Leu	Glu	Gln	Pro	
225					230				235						240	
cta	cat	tta	cac	ctt	tct	att	tat	cct	gaa	cat	aat	aga	att	atc	tta	768
Leu	His	Leu	His	Leu	Ser	Ile	Tyr	Pro	Glu	His	Asn	Arg	Ile	Ile	Leu	
				245					250					255		
cac	tca	tta	cta	gct	gaa	tat	ggg	agc	tgg	tta	ctt	aca	tca	gaa	agt	816
His	Ser	Leu	Leu	Ala	Glu	Tyr	Gly	Ser	Trp	Leu	Leu	Thr	Ser	Glu	Ser	
			260					265					270			
att	gaa	gta	tct	aat	gag	caa	tta	aaa	gga	aat	att	tta	tta	aaa	tat	864
Ile	Glu	Val	Ser	Asn	Glu	Gln	Leu	Lys	Gly	Asn	Ile	Leu	Leu	Lys	Tyr	
		275					280					285				
aat	gga	gaa	gct	act	cat	caa	ctt	cct	ata	aaa	aaa	ctt	aac	tca	tca	912
Asn	Gly	Glu	Ala	Thr	His	Gln	Leu	Pro	Ile	Lys	Lys	Leu	Asn	Ser	Ser	
	290					295					300					
att	acc	ctc	agt	ggc	tca	cta	aat	aaa	cct	aat	ttt	agt	ata	caa	atg	960
Ile	Thr	Leu	Ser	Gly	Ser	Leu	Asn	Lys	Pro	Asn	Phe	Ser	Ile	Gln	Met	
305					310					315					320	
aca	tta	cct	gaa	att	aac	att	aca	aaa	aac	ata	ata	gat	ctt	caa	aca	1008
Thr	Leu	Pro	Glu	Ile	Asn	Ile	Thr	Lys	Asn	Ile	Ile	Asp	Leu	Gln	Thr	
				325					330					335		
gaa	ctt	gtt	att	aat	cta	gga	ctt	ttc	tct	act	cac	tct	gat	att	ctt	1056
Glu	Leu	Val	Ile	Asn	Leu	Gly	Leu	Phe	Ser	Thr	His	Ser	Asp	Ile	Leu	
		340						345					350			
aca	tct	ggg	aca	att	aca	gta	cag	gga	gaa	act	ata	ccc	aat	agt	att	1104
Thr	Ser	Gly	Thr	Ile	Thr	Val	Gln	Gly	Glu	Thr	Ile	Pro	Asn	Ser	Ile	
		355				360						365				
ctt	tcc	agt	gca	gtt	gat	ata	ata	gcc	tct	aca	aca	aca	cat	aca	att	1152
Leu	Ser	Ser	Ala	Val	Asp	Ile	Ile	Ala	Ser	Thr	Thr	Thr	His	Thr	Ile	
	370					375					380					
acc	tta	gag	cat	gca	acc	tta	aca	tct	cca	gaa	atg	cat	ttt	tcc	cta	1200
Thr	Leu	Glu	His	Ala	Thr	Leu	Thr	Ser	Pro	Glu	Met	His	Phe	Ser	Leu	
385					390					395					400	
tct	gga	gaa	ttt	aat	agt	ctt	cta	gga	aat	atc	gat	gca	aac	cta	aaa	1248
Ser	Gly	Glu	Phe	Asn	Ser	Leu	Leu	Gly	Asn	Ile	Asp	Ala	Asn	Leu	Lys	
			405					410					415			
ggg	aat	act	cca	act	ctt	agt	ata	ttt	tct	tct	ctt	ctt	gga	cta	cct	1296
Gly	Asn	Thr	Pro	Thr	Leu	Ser	Ile	Phe	Ser	Ser	Leu	Leu	Gly	Leu	Pro	
			420					425					430			

gat ctt act ggg caa agt aac att act ata gga tta cac cgt caa ggg	1344
Asp Leu Thr Gly Gln Ser Asn Ile Thr Ile Gly Leu His Arg Gln Gly	
435 440 445	
tct tcc tct tca ata gaa gga aca gca act gtc tca ctt aat aat atg	1392
Ser Ser Ser Ser Ile Glu Gly Thr Ala Thr Val Ser Leu Asn Asn Met	
450 455 460	
aac tgg gga gta caa gca tta cag ggg aca tta ggt gat aat gca act	1440
Asn Trp Gly Val Gln Ala Leu Gln Gly Thr Leu Gly Asp Asn Ala Thr	
465 470 475 480	
cta agt gga ata tat aat tta act ccc ata gac tgg tct att tct tta	1488
Leu Ser Gly Ile Tyr Asn Leu Thr Pro Ile Asp Trp Ser Ile Ser Leu	
485 490 495	
aac aaa ttg aaa tta aca gca aag aat gtt tat gct gaa ggc ctt att	1536
Asn Lys Leu Lys Leu Thr Ala Lys Asn Val Tyr Ala Glu Gly Leu Ile	
500 505 510	
aat ttt caa aaa aaa tac ata gat agc tct ata aat ctt ata att cct	1584
Asn Phe Gln Lys Lys Tyr Ile Asp Ser Ser Ile Asn Leu Ile Ile Pro	
515 520 525	
aac ctt cag cta ata gct cct cct ata tct gga gag tta caa tcc tta	1632
Asn Leu Gln Leu Ile Ala Pro Pro Ile Ser Gly Glu Leu Gln Ser Leu	
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Ile Thr Val Ser Gly Lys Leu Asp Ala Pro Ser Ile Glu Ser Lys Ile	
545 550 555 560	
ttt tca tca caa ctc acc tgg aat gcg ctc caa ctt aat aat cct caa	1728
Phe Ser Ser Gln Leu Thr Trp Asn Ala Leu Gln Leu Asn Asn Pro Gln	
565 570 575	
ctc ata ata act act act caa tct tct tcc tct gcg att aaa ggt aat	1776
Leu Ile Ile Thr Thr Thr Gln Ser Ser Ser Ser Ala Ile Lys Gly Asn	
580 585 590	
ata aca ctc tcg gct gag cca gct tca tct gag gca tta acc ttt tca	1824
Ile Thr Leu Ser Ala Glu Pro Ala Ser Ser Glu Ala Leu Thr Phe Ser	
595 600 605	
agt aat tgg gga atc cta cct acg gaa ata cta gta gaa aaa att ata	1872
Ser Asn Trp Gly Ile Leu Pro Thr Glu Ile Leu Val Glu Lys Ile Ile	
610 615 620	
gga aat ata tta gga gta aat ctt gat ggt aat att aaa ata aca aaa	1920
Gly Asn Ile Leu Gly Val Asn Leu Asp Gly Asn Ile Lys Ile Thr Lys	
625 630 635 640	
aaa gat tac ctt ata aat ggt gat att att gca gaa gtt cag tct tgg	1968
Lys Asp Tyr Leu Ile Asn Gly Asp Ile Ile Ala Glu Val Gln Ser Trp	
645 650 655	

aaa gat att gca aac ata ttg caa ata cct att aga ggt tca gca tca	2016
Lys Asp Ile Ala Asn Ile Leu Gln Ile Pro Ile Arg Gly Ser Ala Ser	
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ata aaa ata cag ttt gat cca aag aat caa caa tgt att tct act caa	2064
Ile Lys Ile Gln Phe Asp Pro Lys Asn Gln Gln Cys Ile Ser Thr Gln	
675 680 685	
tgg caa tta aaa aat ttc ata tta ggt aat aat ttt aat gta act act	2112
Trp Gln Leu Lys Asn Phe Ile Leu Gly Asn Asn Phe Asn Val Thr Thr	
690 695 700	
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Ile Lys Gly Arg Ala Asp Thr Ile Gln Leu His Lys Asn Pro Thr Ile	
705 710 715 720	
gct ctc tct tca aaa att ggt gct ggt aca tat gaa gac ttt caa tgg	2208
Ala Leu Ser Ser Lys Ile Gly Ala Gly Thr Tyr Glu Asp Phe Gln Trp	
725 730 735	
aca caa ggg acg tta gac ata aaa ggc aca tta aaa aat ttt aat agt	2256
Thr Gln Gly Thr Leu Asp Ile Lys Gly Thr Leu Lys Asn Phe Asn Ser	
740 745 750	
aaa ata aat ata gca gga caa aca act gta aac gca aac ttt caa aca	2304
Lys Ile Asn Ile Ala Gly Gln Thr Thr Val Asn Ala Asn Phe Gln Thr	
755 760 765	
aat ctt ttt gaa aaa aat att aat ata act act ctt aat tta aaa aat	2352
Asn Leu Phe Glu Lys Asn Ile Asn Ile Thr Thr Leu Asn Leu Lys Asn	
770 775 780	
att caa aaa aat ata gga att aag ctc ctt cag cca ata aaa att ata	2400
Ile Gln Lys Asn Ile Gly Ile Lys Leu Leu Gln Pro Ile Lys Ile Ile	
785 790 795 800	
gtc tca cct caa caa ttt gtt ctt aat aac tgt tca cta gca att ctt	2448
Val Ser Pro Gln Gln Phe Val Leu Asn Asn Cys Ser Leu Ala Ile Leu	
805 810 815	
cca tct gga aca att aca act gat ata tat gtt act cct caa cga ctt	2496
Pro Ser Gly Thr Ile Thr Thr Asp Ile Tyr Val Thr Pro Gln Arg Leu	
820 825 830	
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Asn Ala Asn Ala Ile Ile Lys Glu Val Ser Leu Leu Ser Phe Gln Pro	
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Phe Ser Ile Leu Leu Pro Gln Gly Asn Ile Asn Gly His Ile Thr Leu	
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Thr Gly Ile Pro Ser Lys Pro Lys Gly Thr Leu Ser Phe Asp Ile Leu	

865	870	875	880	
aac ata cat tat cca agg cca aat cca tca ata gca aac tta cat gta				2688
Asn Ile His Tyr Pro Arg Pro Asn Pro Ser Ile Ala Asn Leu His Val	885	890	895	
gaa ggg gaa att ata tct tct cct aac aat ata tgt aaa ctt aat gca				2736
Glu Gly Glu Ile Ile Ser Ser Pro Asn Asn Ile Cys Lys Leu Asn Ala	900	905	910	
acc cta aca gaa aaa aaa gag cct ata cct ata tca ata caa gca aca				2784
Thr Leu Thr Glu Lys Lys Glu Pro Ile Pro Ile Ser Ile Gln Ala Thr	915	920	925	
ctc cct ttt gag ttc aca gaa aac aat atc cct atg cta tct aaa atg				2832
Leu Pro Phe Glu Phe Thr Glu Asn Asn Ile Pro Met Leu Ser Lys Met	930	935	940	
agg cct ttt tct gcc cat atc aag tgg act gga ata tta gat aca ctt				2880
Arg Pro Phe Ser Ala His Ile Lys Trp Thr Gly Ile Leu Asp Thr Leu	945	950	955	960
tgg aaa ctc att cca ctt act gat tac att atg gct ggg aat gga tct				2928
Trp Lys Leu Ile Pro Leu Thr Asp Tyr Ile Met Ala Gly Asn Gly Ser	965	970	975	
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Leu Asp Ala Ser Leu Ser Gly Thr Leu Asp Ser Pro Thr Tyr Ala Ile	980	985	990	
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Ile Thr Thr Leu Ser Asn Ala Asn Phe Gln Asp Leu Ser Leu Gly Leu	995	1000	1005	
tac tta gaa aat atc aat gct aaa tta cag gtc ttt tct aat aga atc				3072
Tyr Leu Glu Asn Ile Asn Ala Lys Leu Gln Val Phe Ser Asn Arg Ile	1010	1015	1020	
tcc cat att caa gct aca gca tct gat ggt aaa caa ggt agt ata caa				3120
Ser His Ile Gln Ala Thr Ala Ser Asp Gly Lys Gln Gly Ser Ile Gln	1025	1030	1035	1040
ctt att ggt aat att ggc tca tct aaa gaa cac ttt cct ttg tct att				3168
Leu Ile Gly Asn Ile Gly Ser Ser Lys Glu His Phe Pro Leu Ser Ile	1045	1050	1055	
aat ggc tcc ttt aca aac ctt gct cca tta caa cgt aaa gac cta agt				3216
Asn Gly Ser Phe Thr Asn Leu Ala Pro Leu Gln Arg Lys Asp Leu Ser	1060	1065	1070	
ctt aca ctt tca gga gca gct act ctt gaa gga aca tta aaa cag tct				3264
Leu Thr Leu Ser Gly Ala Ala Thr Leu Glu Gly Thr Leu Lys Gln Ser	1075	1080	1085	
gaa gtt aaa ggc gat att gtt att aac caa ggc gaa ttt caa ctt act				3312

Glu Val Lys Gly Asp Ile Val Ile Asn Gln Gly Glu Phe Gln Leu Thr	
1090	1095 1100
gaa ggg tta acc agt aat att cca act ctt aat gta gtt gat agc act	3360
Glu Gly Leu Thr Ser Asn Ile Pro Thr Leu Asn Val Val Asp Ser Thr	
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caa caa caa aat aca aag acc aaa aaa gct acc tat caa caa cct acc	3408
Gln Gln Gln Asn Thr Lys Thr Lys Lys Ala Thr Tyr Gln Gln Pro Thr	
1125 1130 1135	
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Leu Ser Ile Ala Leu Ser Ile Pro Asn Arg Phe Phe Val Arg Ser Ser	
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atg ttt gaa agt gag tgg gga ggg aac cta act att aac aaa gtc ata	3504
Met. Phe Glu Ser Glu Trp Gly Gly Asn Leu Thr Ile Asn Lys Val Ile	
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Thr Ser Pro Val Ile Thr Gly Ala Leu Thr Ser Ile Arg Gly Asn Phe	
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Asn Leu Leu Gly Lys Gln Phe Ser Leu Ala Lys Ser Thr Ile Ser Phe	
1185 1190 1195 1200	
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Ser Gly Ser Val Pro Pro Asn Pro Leu Leu Asn Ile Ser Leu Thr Tyr	
1205 1210 1215	
tca tca cct tct att aca gct ata ggc att att aaa ggt aca act agt	3696
Ser Ser Pro Ser Ile Thr Ala Ile Gly Ile Ile Lys Gly Thr Thr Ser	
1220 1225 1230	
aat cct aat att act ttt tca agt aca cca cct tta cct caa gat gaa	3744
Asn Pro Asn Ile Thr Phe Ser Ser Thr Pro Pro Leu Pro Gln Asp Glu	
1235 1240 1245	
ata gtt tcc caa gtt ctt ttt ggt aaa agc tca caa agt ctt agc agg	3792
Ile Val Ser Gln Val Leu Phe Gly Lys Ser Ser Gln Ser Leu Ser Arg	
1250 1255 1260	
ata caa gcc ata caa ctt gct caa gaa tta gca aac tta aca gga ttt	3840
Ile Gln Ala Ile Gln Leu Ala Gln Glu Leu Ala Asn Leu Thr Gly Phe	
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aat act gga agt atg aat ttc cta aca aat att cga cag aca tta ggg	3888
Asn Thr Gly Ser Met Asn Phe Leu Thr Asn Ile Arg Gln Thr Leu Gly	
1285 1290 1295	
tta gat ata ctt agc tta ggg aca act tct aat aga aaa gcc aat aca	3936
Leu Asp Ile Leu Ser Leu Gly Thr Thr Ser Asn Arg Lys Ala Asn Thr	
1300 1305 1310	

tcc aac tca aac gat caa ata gaa gat atc cct gtt ata gaa cta ggt	3984
Ser Asn Ser Asn Asp Gln Ile Glu Asp Ile Pro Val Ile Glu Leu Gly	
1315 1320 1325	
aaa tat att aca gac act gtt tat gtt ggt gtt gaa caa agt tat tta	4032
Lys Tyr Ile Thr Asp Thr Val Tyr Val Gly Val Glu Gln Ser Tyr Leu	
1330 1335 1340	
gat agt aat gat act ggg gca aga ata tca gtt gaa ctt gca cct aat	4080
Asp Ser Asn Asp Thr Gly Ala Arg Ile Ser Val Glu Leu Ala Pro Asn	
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ttt aat ctt gaa ggt aga aca ggg act caa tat agt gag ata ggt att	4128
Phe Asn Leu Glu Gly Arg Thr Gly Thr Gln Tyr Ser Glu Ile Gly Ile	
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Asn Trp Lys Lys Asp Tyr	
1380	

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Ala	Phe	Thr	Leu	Phe	Leu	Gly	Leu	Ile	Ile	Thr	Gly	Ile	Leu	Phe	Ile		
			20					25					30				
Arg	Thr	Ser	Thr	Gly	Ile	Ala	Trp	Ile	Lys	Asn	Thr	Val	Ser	Ser	Leu		
		35					40					45					
Leu	Gln	Gln	Gln	Gly	Ile	Ile	Leu	Gln	Val	Ser	Ser	Ile	Ile	Gly	Pro		
		50				55					60						
Phe	Pro	Glu	Gln	Ile	Thr	Ile	Asn	Glu	Leu	Ser	Leu	Ser	Asp	Val	Asn		
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Gly	Thr	Tyr	Leu	Thr	Ile	Ser	Asn	Leu	Glu	Ile	Gln	Ser	Asn	Leu	Trp		
				85					90					95			
Ala	Leu	Phe	Lys	Gly	Gln	Leu	Glu	Ile	Leu	Ser	Phe	Glu	Leu	Asn	Asp		
			100					105					110				
Leu	Val	Leu	Tyr	Arg	Leu	Pro	Ser	Asn	Asn	Asn	Leu	Lys	Lys	Ser	Ser		
		115				120						125					
Thr	Ser	Phe	Val	Leu	Pro	His	Ile	Ser	Phe	Asp	Leu	Thr	Pro	Trp	Trp		
		130				135					140						
Thr	Glu	His	Ile	Arg	Ile	Gln	Asn	Ile	His	Ile	Asn	Asn	Thr	Gln	Leu		
145					150				155					160			
Ser	Ser	Asp	Ile	Ile	Gly	Ile	Pro	Leu	Val	Leu	Ser	Leu	Glu	Gly	Asp		
				165					170					175			
Gly	Thr	Leu	Thr	Asn	Trp	Asn	Gly	Thr	Phe	Gln	Leu	Ser	Ser	Ser	Asn		
			180				185						190				
Lys	Thr	Lys	Ile	Ile	Gly	Thr	Leu	Arg	Tyr	Gln	Gly	Asn	Lys	Thr	Gln		
		195					200					205					
Phe	Phe	Glu	Tyr	Val	His	Pro	Thr	Arg	Ile	Val	Thr	Leu	Glu	Ile	Asp		
		210				215					220						

Ser	Val	Ala	Asp	Lys	Lys	Ser	Tyr	Asn	Asn	Ser	Ile	Leu	Glu	Gln	Pro	225	230	235	240
Leu	His	Leu	His	Leu	Ser	Ile	Tyr	Pro	Glu	His	Asn	Arg	Ile	Ile	Leu	245	250	255	
His	Ser	Leu	Leu	Ala	Glu	Tyr	Gly	Ser	Trp	Leu	Leu	Thr	Ser	Glu	Ser	260	265	270	
Ile	Glu	Val	Ser	Asn	Glu	Gln	Leu	Lys	Gly	Asn	Ile	Leu	Leu	Lys	Tyr	275	280	285	
Asn	Gly	Glu	Ala	Thr	His	Gln	Leu	Pro	Ile	Lys	Lys	Leu	Asn	Ser	Ser	290	295	300	
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Thr	Leu	Pro	Glu	Ile	Asn	Ile	Thr	Lys	Asn	Ile	Ile	Asp	Leu	Gln	Thr	325	330	335	
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Thr	Ser	Gly	Thr	Ile	Thr	Val	Gln	Gly	Glu	Thr	Ile	Pro	Asn	Ser	Ile	355	360	365	
Leu	Ser	Ser	Ala	Val	Asp	Ile	Ile	Ala	Ser	Thr	Thr	Thr	His	Thr	Ile	370	375	380	
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Ser	Gly	Glu	Phe	Asn	Ser	Leu	Leu	Gly	Asn	Ile	Asp	Ala	Asn	Leu	Lys	405	410	415	
Gly	Asn	Thr	Pro	Thr	Leu	Ser	Ile	Phe	Ser	Ser	Leu	Leu	Gly	Leu	Pro	420	425	430	
Asp	Leu	Thr	Gly	Gln	Ser	Asn	Ile	Thr	Ile	Gly	Leu	His	Arg	Gln	Gly	435	440	445	
Ser	Ser	Ser	Ser	Ile	Glu	Gly	Thr	Ala	Thr	Val	Ser	Leu	Asn	Asn	Met	450	455	460	
Asn	Trp	Gly	Val	Gln	Ala	Leu	Gln	Gly	Thr	Leu	Gly	Asp	Asn	Ala	Thr	465	470	475	480
Leu	Ser	Gly	Ile	Tyr	Asn	Leu	Thr	Pro	Ile	Asp	Trp	Ser	Ile	Ser	Leu	485	490	495	
Asn	Lys	Leu	Lys	Leu	Thr	Ala	Lys	Asn	Val	Tyr	Ala	Glu	Gly	Leu	Ile	500	505	510	
Asn	Phe	Gln	Lys	Lys	Tyr	Ile	Asp	Ser	Ser	Ile	Asn	Leu	Ile	Ile	Pro	515	520	525	
Asn	Leu	Gln	Leu	Ile	Ala	Pro	Pro	Ile	Ser	Gly	Glu	Leu	Gln	Ser	Leu	530	535	540	
Ile	Thr	Val	Ser	Gly	Lys	Leu	Asp	Ala	Pro	Ser	Ile	Glu	Ser	Lys	Ile	545	550	555	560
Phe	Ser	Ser	Gln	Leu	Thr	Trp	Asn	Ala	Leu	Gln	Leu	Asn	Asn	Pro	Gln	565	570	575	
Leu	Ile	Ile	Thr	Thr	Thr	Gln	Ser	Ser	Ser	Ser	Ala	Ile	Lys	Gly	Asn	580	585	590	
Ile	Thr	Leu	Ser	Ala	Glu	Pro	Ala	Ser	Ser	Glu	Ala	Leu	Thr	Phe	Ser	595	600	605	
Ser	Asn	Trp	Gly	Ile	Leu	Pro	Thr	Glu	Ile	Leu	Val	Glu	Lys	Ile	Ile	610	615	620	
Gly	Asn	Ile	Leu	Gly	Val	Asn	Leu	Asp	Gly	Asn	Ile	Lys	Ile	Thr	Lys	625	630	635	640
Lys	Asp	Tyr	Leu	Ile	Asn	Gly	Asp	Ile	Ile	Ala	Glu	Val	Gln	Ser	Trp	645	650	655	
Lys	Asp	Ile	Ala	Asn	Ile	Leu	Gln	Ile	Pro	Ile	Arg	Gly	Ser	Ala	Ser				

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ctcctttaca aaccttgctc c 21

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<220>
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<400> 21
gctcatctaa agaacacttt cc 22

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caaggtagta tacaacttat tgg 23

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gacctaagtc ttacactttc agg 23

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gtattaatac tacattagtt gacg 24

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21

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22

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24

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19

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21

<210> 30

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22

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22

<210> 32

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20

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<400> 45

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21

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23

<210> 47

<211> 29

<212> DNA

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<223> oligo

<400> 47

gaccatggaa aaagtatgtt attttttttc

29

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36

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 <210> 58
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caacgtggat ccgaattcaa gcttc

25

<210> 61

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<212> PRT

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<220>

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<400> 61

Met	Gly	Ser	Gly	Ser	Gly	Asp	Asp	Asp	Asp	Lys	Leu	Ala	Leu	Leu	Thr
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<210> 62

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

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<400> 62

Ala	Thr	Ser	Ile	Thr	Thr	Ser
1				5		

<210> 63

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide

<400> 63

Met	His	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro	Arg	Gly	Ser
1				5					10					15	
Gly	Met	Lys	Glu	Thr	Ala	Ala	Ala	Lys	Phe	Glu	Arg	Gln	His	Met	Asp
			20					25				30			
Ser	Pro	Asp	Leu	Gly	Thr	Asp	Asp	Asp	Asp	Lys	Ala	Met			
		35					40					45			

<210> 64

<211> 50

<212> PRT

<213> Artificial Sequence

<220>

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<400> 64
Met His His His His His His Ser Ser Gly Leu Val Pro Arg Gly Ser
1 5 10 15
Gly Met Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln His Met Asp
20 25 30
Ser Pro Asp Leu Gly Thr Asp Asp Asp Asp Lys Ala Met Ala Asp Ile
35 40 45
Gly Ser
50

<210> 65
<211> 7
<212> PRT
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<400> 65
Glu Phe Asn Leu Ser Lys Gly
1 5

<210> 66
<211> 17
<212> PRT
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<400> 66
Met Gly Ser Gly Ser Gly Asp Asp Asp Asp Lys Leu Ala Leu Gly His
1 5 10 15
Met

<210> 67
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<400> 67
Arg Thr Ser Thr Gly Ile Ala
1 5

<210> 68
<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide

<400> 68

Asp	Pro	Asn	Ser	Ser	Ser	Val	Asp	Lys	Leu	Ala	Ala	Ala	Leu	Glu	His
1				5					10					15	
His	His	His	His	His											
				20											